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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human STRAP-2 prot	Human prostate gro	Human STRAP-1 prot	Kidney injury asso	Human STRAP-4 prot	Human secreted pro	Human STRAP-3 prot	FSHR. Homo sapien	FSH receptor. Hom	FSH receptor, Hom	Human STRAP-1 pept	Human 5' EST secre
	ID	Y58195	Y52589	Y58194	W86309	Y58197	Y95017	Y58196	R27558	R42082	W14782	Y58199	X11840
	DB	21	21	21	20	21	21	21	13	14	18	21	20
	Query Match Length DB	173	141	339	339	128	132	128	695	695	695	34	92
dР	Query Match	38.3	31.3	30.5	29.6	14.5	13.8	10.5	4.6	4.6	4.6	4.6	4.6
	Score	901	736	717	695	341	324	248	107.5	107.5	107.5	107	107
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Y12304 Y54039 R22667 Y70344 W51253 W51251 R21409 R08038	R30524 Y54040 R30517 Y54096 Y43798 Y56088	R30505 Y79251 Y83935 Y20061 WS1252 R30520	W49026 R30509 R41362 W37441 W37427 Y78946 Y34691
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## ALIGNMENTS

Serpentine transmembrane antigen of the prostate; STRAP-2; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; antigen; immunisation; immune response; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug targetting; recombinant protein Y58195 . ID Y58195 standard, Protein; 173 AA Human STRAP-2 protein (portion). 98US-0087520. 98US-0091183. 99WO-US12157 (first entry) (UROG-) UROGENESYS INC (HUBE/) HUBERT R S. (LEON/) LEONG K. (RAIT/) RAITANO A B. (SAFF/) SAFFRAN D C. AFAR D E. HUBERT R S. Homo sapiens. WO9962941-A2. 01-JUN-1999; 01-JUN-1998; 30-JUN-1998; 14-MAR-2000 09-DEC-1999. (AFAR/) Y58195;  (first entry)

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STRAP-2 (serpentine transmembrane antigen of the prostate). STRAP-2 is highly homologous to STRAP-1 (758194), particularly throughout the predicted transmembrane domains, but is encoded by a distinct gene, localised to chromosome 7421. STRAP-1 is the prototype member of the STRAP family of proteins (Y58194-Y58197) which exhibit a high degree of structural conservation, but which show no significant structural homology to known human proteins. STRAP-1 is characterised by six transmembrane domains and intracellular N- and C-termini, suggesting that it folds in a "serpentine" manner into three extracellular and two intracellular loops. STRAP-2 exhibits a markedly different mRNA and protein expression profile relative to STRAP-1. suggesting that these two STRAP-2 expression is not detected in a variety of normal tissues. STRAP-2 expression is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           downregulated in some prostate cancers, whereas STRAP-1 expression remains at a high level. In non-prostate cancers, STRAP-2 expression is generally absent. The function of the STRAP proteins is not known. They may be ion channels (from the presence of six transmembrane domains, a feature which is shared by certain ion channels) or gap-junction proteins (from immunohistochemical staining). STRAP-1 and STRAP-2 are cell-surface tumour antigens. Immunisation with a STRAP protein induces cellular and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for detection, prognosis, and monitoring of cancers (or susceptibility to cancer), as therapeutic inhibitors or to target therapeutic agents to their site of action. STRAP nucleic acids may be used for recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 humoral immune responses against STRAP-expressing cells. STRAP proteins may be used to identify specific-binding agents, to produce anticancer vaccines and to generate specific antibodies. The antibodies may be used
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                                                                                                                                   Novel proteins useful as diagnostic markers and therapeutic targets,
                                                                                                                                                                                                                                                                            sequence represents a portion of a novel human protein,
  Saffran DC;
  Raitano AB,
                                                                                                                                                                     particularly for prostatic cancer
  Leong K,
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                                                  2000-072832/06
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173 AA

Seguence

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or prevent a PGAMP proteins, in gene therapy (e.g., as antisense molecules, triplexforming molecules and ribozymes), and as diagnostic probes and primers. Anti-PGAMP antibodies may be used for diagnosis and monitoring of PGAMP-related diseases by standard immunoassays, as therapeutic antagonists (including targetted delivery of other drugs), and in competitive drug screens. PGAMP-1. Nucleotides encoding PCAMP-1 were initially identified in a prostate cDNA library, this sequence representing a consensus. Human prostate growth associated membrane proteins PGAMP-1 and PGAMP-2 (Y55590) may be used to raise specific antibodies and to screen for specific modulators (agonists, antagonists or other potential therapeutic agents). Antagonists of PGAMP are used to treat or prevent polycystic New human prostate growth-associated membrane proteins, for treating preventing cancer and reproductive disorders wide range of cancers (solid tumours, leukaemia, lymphoma etc.) and reproductive disorders (such as infertility, endometriosis, polycysti ovarian syndrome, prostatitis). PGAMP-encoding nucleic acids, its fragments and complements, may be used for recombinant production of Prostate growth-associated membrane protein; PGAMP-1; prostate; consensus; antibody; screening; modulator; agonist; antagonist; therapeutic agent; cancer; solid tumour; leukaemia; lymphoma; reproductive disorder; infertility; endometriosis; proproductive disorder; infertility; endometriosis; polygystic ovarian syndrome; prostatitis; recombinant expression; gene therapy; antisense therapy; ribozyme; diagnosis; monitoring; immunoassay; targetting; drug delivery; drug screening. This sequence represents human prostate growth-associated protein /note= "Phosphorylated by protein kinase C" /note= "Phosphorylated by casein kinase II" /note= "Phosphorylated by tyrosine kinase" 117..135 Human prostate growth-associated membrane protein PGAMP-1. "Transmembrane domain 1" /note= "Transmembrane domain 3" 81. 102 /note= "Transmembrane Location/Qualifiers Corley NC; Claim 1; Fig 1; 72pp; English. 98US-0083521. (INCY-) INCYTE PHARM INC. /note= Guegler KJ, WPI; 2000-062671/05 N-PSDB; Z46296 Modified-site Modified-site Modified-site 22-MAY-1998; sapiens WO9961469-A2 17-MAY-1999; 02-DEC-1999, Lal P, Domain Domain Domain Homo Key 

141 AA; Sequence

Y52589 standard; Protein; 141 AA

RESULT

Y52589

Y52589 ID YE XX AC YE

ö Gaps ; Length 141; Indels 31.3%; Score 736; DB 21; 100.0%; Pred. No. 9.7e-72; iive 0; Mismatches 0; Conservative Best Local Similarity Matches 141; Conserv Query Match

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                                                                                                                                                         transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; pancreatic cancer; ovarian cancer; tumour antigen; immunisation; immune response; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug targetting; recombinant protein.
433
                               Serpentine transmembrane antigen of the prostate; STRAP-1; prostate;
                          LAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFV
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te= "Extracellular region 2 (Y58199)"
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e= "Extracellular region 3 (Y58200)"
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.e= "Transmembrane domain 5"
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(HUBE/) HUBERT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
                                                                                                                                                                                                                                      Leong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1A; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Z49395, Z49396.
                                                                                                                                                                                                                                      Hubert RS,
(LEON/) LEONG K.
(RAIT/) RAITANO A B.
(SAFF/) SAFFRAN D C.
                                                                                                                                                                                                                                                                                                                                                         2000-072832/06
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셤 ò

328 SERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVŢSIPSVSNALN

268 SLVYLAGLLAAAYQLYYGTKYRRFPPWLEFWLQCRKQLGLLSFFFAMVHVAYSLCLPMRR 327

Page

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The present sequence represents a kidney injury associated molecule

(KIM) protein. KIM proteins can be administered therapeutically
by expressing KIM encoding polynuclecities, to promote growth and/or
survival of damaged tissue (e.g. renal tissue), since the KIM proteins
are upregulated in injured or regenerating (especially renal) tissues.

KIM fusion proteins, conjugates, antibodies and vectors can also be used
therapeutically, e.g. these or the KIM proteins may be included with an
acceptable carrier in pharmaceutical compositions, useful for therapy/
prophylaxis of conditions associated with disfunction/disregulation of
KIM genes or proteins, especially renal diseases or impairments of renal
function in humans (e.g. acute renal failure, acute nephritis). The
polynuclecitides can be used to produce antisense sequences which, when
internalised into cells, can disrupt expression of a cellular KIM gene,
also useful in therapy (e.g. to block the growth of tumours dependent or
compositions. The proteins and polynuclecities are
useful diagnostically e.g. to detect and quantify renal injury or impaired
tindicative of increased risk, or presence of, renal injury or impaired
tinsue growth arising from/affecting renal tissue). The proteins can
also be used to locate KIM-producing cells (especially specific loci,
also be used to locate KIM-producing cells (especially specific loci,
arising from/affecting renal tissue). By contacting cells with an
imageable KIM-binding reagent and imaging reagent accumulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growth and regeneration, especially to treat renal conditions
                                                                                                                                                                                     Kidney injury associated molecule; kidney injury related molecule; KIM; tissue growth promotion; regeneration; renal condition; acute renal failure; acute nephritis; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ξ
                                                                                                                                                   Kidney injury associated molecule HW018 protein.
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                                W36309 standard; Protein; 339 AA
                                                                                                                                                                                                                                                                                                                                                                                     98WO-US10547.
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                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                        W09853071-A1.
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W86309
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388 WREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSIVILDLL 447
                                                                                                                                                                                                                      Serpentine transmembrane antigen of the prostate; STRAP-4; placenta; transmembrane domain; type IIIa membrane protein; expression; cancer; antigen; immunisation; immune response; cellular; humoral; prostate; anticancer vaccine; antibody; detection; diagnosis; liver; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug targetting; recombinant protein; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel proteins useful as diagnostic markers and therapeutic targets, particularly for prostatic cancer
Human STRAP-4 protein, encoded by placenta EST R80991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saffran DC;
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                                                                                                                                                                                                                                                                                                                                                                           "Encoded by CTN"
                                                                                                                                                                                                                                                                                                                                                                                                                    "Encoded by NTC"
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                                                                                                                                                                                                                                                                                                                                                                                               by
                                                                                                                                         Y58197 standard; Protein; 128 AA.
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98US-0091183.
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122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAITANO A B.
SAFFRAN D C.
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HUBERT R S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-072832/06.
N-PSDB; Z49402.
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                                                                    448 QLC 450
                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                       307 vic 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAFF/)
                                                                                                                                                            Y58197;
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Length 339;

29.6%; Score 695; DB 20; Length 3 52.3%; Pred. No. 1e-66; ive 52; Mismatches 64; Indels

127; Conservative

Matches

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Best Local Similarity

Query Match

208 LFTLWRGPVVVAISLATFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLL 267

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This sequence represents a novel human protein, STRAP-4

(serpentine transmembrane antigen of the prostate) encoded

by human placenta EST (expressed sequence tag) R80991. STRAP-4 is

a transmembrane protein closely related to STRAP-1 (YS8194) and

STRAP-2 (YS8194) and

STRAP-2 (YS8195), but it is predominantly expressed in liver

tissue. The STRAP-1 is the prototype member of the STRAP family of proteins

(YS8194-YS8197) which exhibit a high degree of structural conservation,

tysue. STRAP-1 is characterised by six transmembrane domains and

proteins. STRAP-1 is characterised by six transmembrane domains and

intracellular N- and C-termini, suggesting that it folds in a

intracellular n- and C-termini, suggesting that it folds in a

cloops. The function of the STRAP proteins is not known. They may be

ion channels (from the presence of six transmembrane domains, a feature

which is shared by certain ion channels) or aga-junction proteins

tumour antigoners. Imminisation with a STRAP-1 and STRAP-2 are cell-surface

tumour antigoners.
                                                                                                                                                                                                                                                                                                                                                                                                                                           humoral immune responses against STRAP-expressing cells. STRAP proteins may be used to identify specific-binding agents, to produce anticancer vaccines and to generate specific antibodies. The antibodies may be used for detection, prognosis, and monitoring of cancers (or susceptibility to cancer), as therapeutic inhibitors or to target therapeutic agents to protein production, and amonitoring of sancers (or susceptibility to remine in a feation. STRAP nucleic acids may be used for recombinant protein production, and anguestic and prognostic reagents, for identifying STRAP-expressing cells for screening inhibitors of STRAP expression and for therapeutic modulation/inhibition of STRAP expression. Since high levels of STRAP proteins are exposed on the cell surface, they are easily targetted by systemically administered agents, and because they are expressed mainly on prostatic epithelial cells, agents targetted to them should have minimal side effects on other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          blood disorder; heemophilia; autoimmune disease; diabetes; inflammation; infection; fungal; bacterial; viral; HIV; allergy; arthritis; neurodegenerative disease; asthma; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; cancer; tumour; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 128; Score 341; DB 21; Length 128; Best Local Similarity 61.3%; Pred. No. 4.2e-29; Matches 57; Conservative 20; Mismatches 16; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein vp17_1, SEQ ID NO:74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 HVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSI 441
                     Example 5; Fig 11B; 83pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 AA;
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secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following: cytokine activity: cell proliferation; differentiation; immune modulation; haematopolesis regulation; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic and tumour inhibition thrombolytic activity; anti-inflammatory activity; and tumour inhibition activity. The proteins may be administered to patients as vaccines, and the nucleotides may be treated using the proteins or nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, capecially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary inflammation; dual labertes syndrome; insulin dependent diabetes and business and allergic reactions such as asthma and anemia. They may
                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to 40 human secreted proteins (Y94981-Y95020), and cDNA sequences encoding them (A23423-A23462). The secreted proteins of the invention include those that are thought to be only partially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       also be used for treating wounds, burns, ulcers, osteoporosis, osteoportais, periodontal diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activity may additionally be useful as contraceptives. Nucleic acid sequences of the invention may be used in chromosome mapping, and as a source of diagnostic priners and probes. The present sequence represents one of the 40 proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 IEMYISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWK 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
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                                                                                                                                                                                                                   Hoffman H, Hall J,
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                                                                                                                                                                                                                                                                                                                                                                    Claim 83; Page 334; 357pp; English.
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rafeesrykfylpptftltllvpcvvil
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           98US-0097639.
98US-00997659.
98US-01090918.
98US-010978.
98US-0113645.
99US-0379246.
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                                                                                                                                                                                                                   Valenzuela D, Yuan O,
                                                                                                                                                                                  (ALPH-) ALPHAGENE INC
                                                                                                                                                                                                                                                                                                                                 diseases and cancer -
                                                                                                                                                                                                                                                       WPI; 2000-224657/19.
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                                                                                   25-NOV-1998;
23-DEC-1998;
23-DEC-1998;
                                                09-SEP-1998;
28-SEP-1998;
               24 - AUG - 1998;
24 - AUG - 1998;
                                                                                                                                             23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
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Y58196
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Human STRAP-3 protein, encoded by testis EST AI139607.

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Length 128;

Query Match

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N-PSDB; 249401
             Homo sapiens
                WO9962941-A2
                      01-JUN-1999;
                         01-JUN-1998;
                   09-DEC-1999
                              (UROG-)
(AFAR/)
                                    (RAIT/)
(SAFF/)
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                                   LEON/)
                                 HUBE/
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Best RESULT R27558 a δ q This sequence transmembrane antigen of the prostate) encoded by human testis EST (expressed sequence tag) Al139607. STRAP-3 is a transmembrane protein closely related to STRAP-1 (YSB194) and STRAP-2 (YSB195), but its expression is predominantly restricted to placenta although there is a smaller degree of expression in normal prostate tissue. It does not appear to be expressed in other normal prostate or proteins and prostate cancer. The STRAP-3 gene has been localised to chromosome 7921. STRAP-1 is the prototype member of the STRAP family of proteins of the prototype member of the STRAP family of proteins of the aracterised by six transmembrane domains and proteins. STRAP-1 is characterised by six transmembrane domains and chromosome contracted by a significant structural homology to known human contracted by a six transmembrane domains and chromosome contracted by a six transmembrane domains and shared by certain to three extracellular and two intracellular contracted by six transmembrane domains. They may be soon of the STRAP proteins is not known. They may be contracted by certain ion channels) or gap-juction proteins contracted by certain ion channels) or gap-inction proteins contracted by certain to three stransmembrane domains.

(From immunohistochemical staining) is STRAP-1 and STRAP-2 are cell-surface tumour antigens. Immunisation with a STRAP-expressing cells. STRAP proteins may be used to identify specific-binding agents, to produce anticancer vaccines and to generate specific antibodies. The antibodies may be used for detection, prognosis, and monitoring of cancers (or susceptibility to cancer), as therapeutic inhibitors or to target therapeutic agents to their site of action. STRAP nucleic acids may be used for recombinant identifying STRAP-expressing cells for screening inhibitors of STRAP expression and for therapeutic modulation/inhibition of STRAP expression. Since high levels of STRAP proteins are exposed on the cell surface, they are easily targetted by systemically administered agents, and because they are expressed mainly on prostatic epithelial cells, agents targetted to them should have minimal side effects on other Scrpentine transmembrane antigen of the prostate; STRAP-3; placenta; transmembrane domain; type IIIa membrane protein; expression; cancer; antigen; immunisation; immune response; cellular; humoral; prostate; anticancer vaccine; antibody; detcrion; diagnosis; testis; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug targetting; recombinant protein; expressed sequence tag; EST. Novel proteins useful as diagnostic markers and therapeutic targets, protein production, as diagnostic and prognostic reagents, for Leong K, Raitano AB, Saffran DC; This sequence represents a novel human protein, STRAP-3 Example 5; Fig 11B; 83pp; English particularly for prostatic cancer 99WO-US12157. 98US-0087520. UROGENESYS INC Afar DE, Hubert RS, RAITANO A B. SAFFRAN D C. WPI; 2000-072832/06 AFAR D E. HUBERT R S. 128 AA; LEONG K. Seguence

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346 ENSWNEEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLI 405
                    Gaps
                                              Pure human FSH receptor, fragments and mutants - for preventing follicle growth, maturation and spermatogenesis, also for use of appropriate cell lines for bio-assays of FSH
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                                                                                                                                                                                                                 Human; follicle stimulating hormone receptor; maturation; spermatogenesis; birth control.
                   Indels
                                                                                                                                                                                                                                                                                                                       "N-terminal extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "C-terminal intracellular domain"
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                                                                                                                                                                                                                                                                                                                                                                                               "transmembrane region III"
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10.5%; Score 248; DB 21; 44.4%; Pred. No. 4.7e-19;
                                                                         406 STFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSIVIL 444
                                                                                    "transmembrane region II"
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         Pred. No. 4.7e
20; Mismatches
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                                                                                                                                                                                                                                                                                                     "mature hFSHR "
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         Local Similarity
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93WO-EP00780 92EP-0200886

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The primers given in Q50029-34 were used in the cloning of GST-FSH-R1, GST-FSH-R2 and GST-FSH-R3 fusion protein constructs. Screening of the human testis cDNA library with a hFSH-R specific probe resulted in five recombinant phages positive in hybridisation. (Q50013).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibodies, anti-idiotypic antibodies, and transfected cells, useful e.g. in diagnosis and as antidote for FSH overstimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New follicle stimulating hormone receptor - and derived
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                                                                                                     (FSHR) was deduced from the DNA sequence obtd. by screening a lambda gt11 cDNA library constructed from RNA extracted from human testis with a rat FSHR cDNA clone as a probe. HFSHR binds to FSH to reduce endogenous FSH bioactivity, in females to prevent follicle growth and maturation and in males to prevent spermatogenesis, i.e. as a birth bioactivity and in X-ray crystallographic analysis to develop molecular models useful in defining the tertiary structure of the hormone binding domains of HFSHR. This will aid the design of peptides with FSH (ant)agonist activity.
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                                                                           protein sequence of human follicle stimulating hormone receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.6%; Score 107.5; DB 13; Length 695;
17.0%; Pred. No. 0.0098;
ive 77; Mismatches 148; Indels 185;
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Claim 2; Page 25; 48pp; English
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Best Local Similarity 17.09
Matches 84; Conservative
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INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL 181
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                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                          SWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWRE------FSFIQSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---VLIYGWKRAFEEEYYRFYTPPNFV-LA
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                                                                                                                                                                                                                                                                                                   182 ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 vdymtqtrggrsslaednessysrgfdmtytefdydlcnevvdvtcspkpdafnpcedim
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| gynilrvliwfisilaitgniivlvilttsgykltvp----rflmcnlafad-----
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                                                          Length 695;
                                                                                                                                                                                                                                                           157 ih-----tiernsfvglsfesvilwl----nkngigeihnca----
                                                          DB 14;
                                              4.6%; SCOIE ... 0.0090,
17.0%; Pred. No. 0.0090,
*ive 77; Mismatches 148;
                                                                                                                                      HEDALTKTNIIFVAIHREHYTSLWDLRHLLVG----
                                                                                                                                                                                                                                                                                                                                                                                242 NQOSDFYKIPLEIVNKTL-PIVAITLLSLVY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G----LLSFFFAMVHVA----
                                                                                                84; Conservative
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                                                          Query Match
Best Local Similarity
695 AA;
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us-09-455-486-6.rag

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Disclosure; Page 22; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   particularly for prostatic cancer
                                                                                                                                                                  Y58199 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0087520
                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0091183
                                                                                                                                                                                                               (first entry)
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516 iclpmdidsplsql 529
                                                                                      436 LVLPSIVILDLLQL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UROG-) UROGENESYS INC
                                         399 G---YVALLISTFH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hubert RS,
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SAFFRAN D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-072832/06
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HUBERT R S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEONG K.
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                                                                                                                                                                                                              14-MAR-2000
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                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Afar DE,
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                                                                                                                                                                                        Y58199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUBE/)
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                                                                                                                                             RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KILIDVSNNMR 121
                                                                                                                                                                                                                                                                                                                                             Diagnosis of ovarian dysgenesis and carriers from DNA abnormalities - by amplifying DNA including follicle stimulating hormone receptor allele(s), i.e. codon 189, cleaving fragments, and examination
                                                                                                                                                                                                                                                                                                                                                                                                             The human follicle stimulating hormone (FSH) receptor (W14782) is a G-protein coupled transmembrane receptor. A mutation in the fshr gene (see also T63181) is associated with ovarian dysgenesis, and methods for provided for the diagnosis of this disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 · INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 rstynlkklp-----tleklvalmeasltypshccafanwrrgiselhpicnksilrge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 gynilrvliwfisilaitgnlivlvilttsgykltvp----rflmcnlafad-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 in------tiernsfvglsfesvilwl----nkngigeihnca-----
                                                                                                                        hormone receptor; FSH receptor; hypergonadotropic hypogonadism; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.6%; Score 107.5; DB 18;
17.0%; Pred. No. 0.0098;
ative 77; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 HEDALTKTNIIFVAIHREHYTSLWDLRHLLVG------
                                                                                                                                                                                                                                                                                         Huhtaniemi I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 NQQSDFYKIPIEIVNKTL-PIVAITLLSLVY-----
                                                                                                                                                                                                                                                                    (UYHE-) UNIV HELSINKI LICENSING LTD OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----:-LAGLLAAAYQLYYGTKYRRF-
                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 18-21; 43pp; English.
                             W14782 standard; Protein; 695 AA
                                                                                                                                                                                                                                                                                         Aittomaeki K, De La Chapelle A,
                                                                                                                                                                                                                        96WO-FI00501
                                                                                                                                                                                                                                             95US-0531070
                                                                          (first entry)
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                                                                                                                     Follicle stimulating
                                                                                                                                                                                                                                                                                                               WPI; 1997-202900/18.
                                                                                                                                  ovarian dysgenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      695 AA;
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                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                        20-SEP-1996;
                                                                                                                                                                                                                                             20-SEP-1995;
                                                                                                 FSH receptor
                                                                         20-JUN-1997
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Best Local S
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                                                   W14782;
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RESULT 10
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acid protein characterised by six transmembrane domains and intracellular N- and C-termini, suggesting that it folds in a "serpentine" manner into three extracellular and two intracellular loops. STRAP-1 mRNA and protein expression is maintained at high levels and throughout all stages of prostate cancer. STRAP-1 mRNA and/or protein is also overexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the extracellular regions of STRAP-1 (serpentine transmembrane antigen of the prostate, Y58194). These peptides were used to raise monoclonal anti-STRAP-1 antibodies. STRAP-1 is the prototype member of the STRAP family of proteins (Y58194-Y58197) which exhibit a high degree of structural conservation, but which show no significant structural homology to known human proteins. The STRAP-1 gene has been localised to chromosome 7p22. STRAP-1 is thought to be a type IIIa membrane protein and is expressed predominantly in prostate cells in normal human tissues. Structurally, STRAP-1 is a 339 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane domain; type Illa menbrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; pancreatic cancer; ovarian cancer; tumour antiqen; immunisation; immune response; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor; accombinant protein.
456 svytltaitlerwhtithamgldckvqlrhaasvmvmgwifafaaalfpifgissymkvs 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human STRAP-1 peptide, corresponding to STRAP-1 extracellular region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences Y58198-Y58200 represent synthetic peptides that correspond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serpentine transmembrane antigen of the prostate; STRAP-1; prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel proteins useful as diagnostic markers and therapeutic targets,
                                                                                                                                                          ----VLIYGWKRAFEEEYYRFYTPPNFV-LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saffran DC;
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certain other cancers, including bladder, colon, pancreatic and ovarian channels from the presence of six transmembrane domains, a feature which is shared by certain ion channels) or gap-junction proteins which is shared by certain ion channels or gap-junction proteins cancers. Immunohistochemical staining). STRAP-1 and STRAP-2 are cell-surface tumour antigens. Immunoisation with a STRAP protein induces cellular and humoral immune responses against STRAP-expressing cells. STRAP proteins may be used to identify specific-linding agents, to produce anticancer vaccines and to generate specific antibodies. The antibodies may be used for detection, prognosis, and monitoring of cancers (or susceptibility to cancer), as therapeutic inhibitors or to target therapeutic agents to their site of action. STRAP nucleic acids may be used for recombinant of cancer), as diagnostic and prognostic reagents, for identifying STRAP-expressing cells for screening inhibitors of STRAP expression and for therapeutic modulation/inhibition of STRAP expression. Since high levels of STRAP proteins are exposed on the cell surface, they are easily targetted by systemically administered agents, and because they are easily targetted by systemically administered agents, agents, agents targetted to them should have minimal side effects on other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 107; DB 21; Length 34;
Pred. No. 0.00011;
5; Mismatches 9; Indels · 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duclert A, Dumas Milne Edwards J, Lacroix B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human 5' EST secreted protein SEQ ID No: 440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 RRSERYLFLNMAYQQVHANIENSWNEEEVWRIEM 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 34; Page 577; 675pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 58.8
20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 34 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-1998;
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Best Local S
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Y11840
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X40438 to X40715 represent 5' expressed sequence tags (ESTS) for human secreted proteins expressed in prostate, and encode the proteins given in Y1176 to Y11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, haematopolesis regulating activity, itssue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, activity or other activity, anti-inflammatory activity, tumour inhibition activity or other activity, reproducts can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 4.6%; Score 107; DB 20;
46.5%; Pred. No. 0.00052;
ative 8; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 5' EST secreted protein SEQ ID NO:335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; Page 677; 824pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y12304 standard; Protein; 109
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les 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                          Sequence
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amplifying and analysing genes

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                             can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell prolliferation/differentiation activity, haematopolesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy
                                                                                                                                                                             and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endonuclease polynucleotide sequence was modified by substituting codons that are unique to mitochondria (the gene is expressed in mitochondria) with universal codons. The endonuclease cuts molecules within sequence 237078, and is therefore useful in genetic engineering techniques such as PCR (polymerase chain reaction) for cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endonuclease hydrolyses the phosphodiester bond of a polynucleotide chain. The endonuclease is the 50 kDa subunit of a yeast endonuclease. The endonuclease gene was modified so that it could be mass-produced in an expression system such as E. coli or yeast. The
             N-terminal fragment of a secreted protein. The nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SceI endonuclease; phosphodiester bond; yeast; genetic engineering; PCR; polymerase chain reaction; gene cloning.
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                                                                                                                                                                                                                                                                                                                                                    Length 109;
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                                                                                                                                                                                                                                                                                                                                                    Score 102; DB 20; Length 1
Pred. No. 0.0022;
8; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y54039 standard; Protein; 476 AA
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                                                                                                                                                                                                                                                                                                                                                      4.38;
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Best Local Similarity 43.2
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                               109 AA;
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                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                       104 LRHLLVGKILIDVSNNMRINQYPESNAEYLASLF--PDSLIVKGFNVVSAWALQLGPKDA 161
                                                                                                                                                                                                    162 SRQVYICSNNIQARQQVIELARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAIS 221
                                                                                 66; Gaps
                                                                                                                                                                                                                                                  222 LATFFLYSFVRDVIHPYARNQQSDFYKIP----IEIVNKTLPIVAITLLSLVYLAGLLA 277
                                                                                                                                                                                                                                                                        ----fiyyf--dkflplhdnkqfnyikfrfntfiksynwnnrvfglvlse--yinniki 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endonuclease SceI; PAGE; chromatography; ENS2 gene; mitochondria; ss.
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                                                       4.3%; Score 101; DB 21; Length 476; 20.7%; Pred. No. 0.028; iive 48; Mismatches 85; Indels 66
                                                                                                                                                                   62 NPKFASEFFPHVVDVTHHEDALTKTNI----IFVAIHREHYT
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59..64
136..145
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                                                         Query Match
Best Local Similarity 20.7%,
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sacchromyces cerevisae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 kD subunit of Scel.
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                       476 AA;
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281 npyfvnafsini------ktnlakekiftniynklysdykinginnhipyynylk 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 LRHLLVGKILLIDVSNNMRINQYPESNAEYLASLF--PDSLIVKGFNVVSAWALQLGPKDA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 SROVYICSNNIQARQOVIELARQLNFIPIDLGSLSSAREIENL,PLRLFTLWRGPVVVAIS 221
            The sequence given is the 50kD subunit of endonuclease SceI. The sequence is given as it is represented in the specification and it appears to be derived from mitochondrial DNA due to the codon usage. The purpose of the marked domains is unclear. Endonuclease SceI can be mass produced from the 50kD subunits expressed from the ENS2 gene. The 50kD subunit was purified by treating SceI from eg. Sacchromyces IAM4274, and by denaturing the phosphocellulose column.
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4.3%; Score 101; DB 13; Length 503;
Best Local Similarity 20.7%; Pred. No. 0.03;
Matches 52; Conservative 48; Mismatches 85; Indels 6
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